Teaching Portfolio

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Teaching Philosophy

As an evolutionary biologist turned bioinformatician, I understand the importance of adapting to a constantly changing world. Technology and data continuously alter the way we think about and approach questions in biology. Often students come to class expecting there to be a "right answer" to every question and a finite, static knowledge base to learn. The first thing that I convey to my students is that this simply is not true. I do not have all the answers and neither does anyone else. The beauty of biological sciences is that they are dynamic; we are constantly learning something new. As budding scientists, they will shape the field through discovery. Once students realize this, I find that the focus of the class moves from memorizing "facts" to learning how to be competent researchers through inquiry. I feel that my role as a teacher-scientist is to train the next generation of scientific thinkers through exposure to the scientific process allowing them to understand how scientists come to conclusions.

My classroom is a teaching-laboratory. My students spend the semester simultaneously learning a skill set and applying it to answer a real world question. There is an adage amongst bioinformaticians that you cannot truly learn a programming language until you have a problem you need to solve. I feel that this speaks to new scientists in many fields. For example, in my experience as a TA for Molecular Systematics, early in the semester students pose a research question and begin collecting data from online databases. Through the theory learned in class, students use phylogenetic and molecular evolutionary analyses to attempt to answer their question. Previous questions include investigating the relationship between species range and species richness and looking at the loss and gain of bioluminescence in fireflies across a phylogeny. Through this type of active learning environment, students are able to experience scientific inquiry first hand. Since the breadth of scientific knowledge is constantly expanding, we also spend time reading recent papers chosen by students within the general subject area. Students lead discussions over the paper that they choose often generating excellent conversation as they try to grasp what the new research means for themselves as well as the scientific community. Many times, students take what they learn in the papers and apply it to their own projects making them more innovative and much stronger than originally proposed. Many students go on to use what they accomplish in class as part of a larger project they have with a professor and, at times, are even able to publish the results.

I assess student learning through exams, progress reports, presentations and personal conversations. Not all of my assessments are graded. The personal conversations are more of an opportunity for me to see where the student is in their understanding of the material in a very relaxed manner. These conversations help me to gauge with which topics I need to be more explicit. Overall, learning is assessed through the ability of the students to conduct a well thought-out research project and to communicate the results to their colleagues. I also look at how they applied the methods and theories discussed in class to their work. This assessment ensures that students are not just learning a number of different ideas and theories, but that they truly understand how to apply them in the manner intended.

As a teacher-scientist, I feel that it is important to instill the scientific process in my students. Even if they do not go on to become the next great evolutionary biologist, scientific thinking is vital in a world where good science is always under attack. I teach students to think for themselves and to analyze the data of a situation to make their own decisions. The greatest product of my classroom is an individual that can critically consider the barrage of scientific misinformation that bombards them daily creating a truly informed citizen.

Description of Courses Taught

University of Georgia—Department of Plant Biology

Plant Taxonomy (PBIO 4650L/6650L)

Role:	Graduate Laboratory Assistant
Semesters Taught:	Spring 2009, Spring 2011
Enrollment and Student Profile:	~10 students per semester, undergraduate/graduate
Course Type:	Upper level organismal
Course Content:	Identification and classification of plants.

Teaching Responsibilities:
I was one of three laboratory assistants for both semesters taught. This course was the laboratory component of the main lecture course (PBIO 4650/6650) and was designed to incorporate lecture materials while introducing new concepts and aspects of anatomy, taxonomy and evolution of land plants, with primary focus on angiosperms. I taught the same group of students twice a week both semesters, introducing a new laboratory exercise each time. I co-developed the syllabus, quizzes and exams with my fellow LAs. The second time I taught the lab, we developed new lab exercises for approximately half of the classes. The revamping was well received as it better enforced what was taught in lecture while incorporating the goals of the lab for plant identification.

Bioinformatics Applications (PBIO (BIOL) (BINF) 4550/6550)

Role:	Teaching Assistant
Semesters Taught:	Fall 2009
Enrollment and Student Profile:	~30 students per semester, undergraduate/graduate
Course Type:	Upper level interdisciplinary
Course Content:	Application and theory of bioinformatics.

Teaching Responsibilities:
I was a teaching assistant that aided students primarily outside of class through one-on-one tutoring sessions and e-mail correspondence. There were labs built into the class that occurred sporadically, and during these times, I acted as a primary assistant to help students through the lab exercises. I also graded all homework assignments and provided feedback.

Molecular Systematics (PBIO 6350)

Role:	Laboratory Assistant
Semesters Taught:	Spring 2010
Enrollment and Student Profile:	~8 students, graduate
Course Type:	Graduate level
Course Content:	Application and theory of phyloinformatics.

Teaching Responsibilities:
My primary responsibility was to assist students during the laboratory sections, which focused on using different phyloinformatics software to analyze data. I tested and troubleshot labs to make sure that they would work during class. I helped students with homework and general understanding of concepts/program usage outside of class. I also provided feedback and suggestions for their term projects, which included novel analyses of data sets they obtained. I designed and taught a lab on using R for phylogenetic analyses.

Graduate Student Seminar for Teaching Assistants (GRSC 7770)

Role:	Co-instructor
Semesters Taught:	Fall 2011
Enrollment and Student Profile:	15 students, graduate
Course Type:	Graduate seminar
Course Content:	Introduction to teaching pedagogy, services and methods.

Teaching Responsibilities:
As primary instructor of the course, I designed the syllabus and set up invited speakers to come teach about various aspects of teaching and teaching related services available on campus. I also built on previous versions of the class by adding more opportunity for students to present in front of each other, as was suggested by evaluations taken from the previous year's students. Students are tasked with creating a lab introduction, an assessment and rubric, a teaching philosophy statement and an active learning strategy.

Sample Teaching Materials

Rosids I & II—Euphorbiaceae, Brassicaceae & Malvaceae

Today you will be looking at three families in the rosid clade: Euphorbiaceae, Brassicaceae and Malvaceae. Euphorbiaceae is in rosids I (as are Rosaceae and Fabaceae from the previous lab) and is in the order Malpighiales, along with Violaceae (violets), Passifloraceae (passion flowers), and Salicaceae (willows). Brassicaceae and Malvaceae are in rosids II, in the orders Brassicales and Malvales, respectively. Brassicaceae are closely related to Capparaceae (the caper family) while Malvaceae are related to Cistaceae (the rock-rose family), though the exact relationship is unclear.

Euphorbiaceae – the spurge family

Euphorbiaceae is a family of ~300 genera and 7000+ species, making it one of the top ten most speciose plant families. Euphorbiaceae have a cosmopolitan (worldwide) distribution and are particularly prevalent in the old world tropics. While many associate Euphorbiaceae with succulent plants similar to Cactus, these succulent species represent only a small portion of the family and occur only in the old world (Note: Cactaceae are a new world family). Our North American representatives are mostly small non-succulent herbaceous perennials, but all share similar floral morphology and thick, milky (usually) sap. **NOTE: The sap from these species is poisonous. If you get it on your hands, make sure you wash your hands before contacting other parts of your body**.

Manihot (cassava) is a primary food source in tropical and subtropical regions. Other economically important species included *Hevea* (rubber) and *Euphorbia* (poinsettia). *Ricinus communis* (castorbean) is considered one of the most poisonous plants in the world due to the protein, ricin. The largest genera in the United States are *Chamaesyce*, *Euphorbia* and *Croton*.

Answer the following questions using the specimens provided.

1. *Jatropha sp.*
   a. Inflorescence: determine the inflorescence type.
   b. Are the flowers perfect/imperfect? Complete/incomplete? What do you notice about the arrangement of flowers on the inflorescence?
   c. Without removing the pistil, how many carpels do you think are present? What is the ovary position?

2. Euphorbia – species in this genus also posses compound cymes but in a condensed form comprising a unique structure known as a cyathium. Define **cyathium**.

2a. *Euphorbia milii*
   a. Describe the leaf complexity. **Note:** pinch the leaf and you will see milky juice coming out, which is a diagnostic character of this family.
   b. Diagram an inflorescence and include bracts, involucres, nectariferous discs (How many?), pistillate flowers (How many?), and staminate flowers (How many?). Refer to Zomlefer book (drawings on P. 108) for clarification before asking your TA.
   c. Can you determine the number of carpels? If so, how many are there? What is the ovary position?

2b. *Euphorbia pulcherimma* (Poinsettia)
   a. Can you identify the bracts and involucres? How many of each per cyathium do you see?
   b. How many nectariferous discs per cyathium?
   c. How many carpels are present? What is the ovary position?

3. *Codiaeum variegatum*
   a. What is the inflorescence type? Are the flowers perfect or imperfect? Is the plant monoecious or dioecious?
   b. Do you see a perianth? Can you differentiate a calyx and corolla? If so, how many petals and sepals are present?

4. *Croton alabamense*
   a. What is the inflorescence type? Are the flowers perfect or imperfect? Is the plant monoecious or dioecious?
   b. Do you see a perianth (Do not remove flowers)? Can you differentiate a calyx and corolla? How many petals and sepals are present?

One of the labs that I co-wrote for Plant Taxonomy (PBIO 4650/6650) for Spring 2011. In this portion, students explored the morphological traits used to circumscribe the angiosperm family Euphorbiaceae. A major challenge of this lab was getting the students to understand the complex inflorescence structure, the cyathium. Once all students completed that portion of the lab, we worked together using a dissecting scope, a live specimen and drawings on the chalkboard to describe all the portions of this unique inflorescence type.

In this assignment from Bioinformatics Applications (PBIO 4550/6550), students had to create a website by writing the HTML themselves.

Student's Website and Original Code:


```
<html><!--webpage begins with this tag-->
<head><!--head tag-->
<title>Clover's Christmas Budget</title><!--this is what will appear in the address bar-->
</head>
<body bgcolor="#ccffcc"><!--inside this tag you will write the contents of your webpage-->
<h1 align="center"><!--to tell the browser alignment of your content--><font face="Arial Narrow"><b><font size="6"><!--tell the browser the
fonts of your contents, here I use the text frot as Arial Narrow, bold and size 6-->Christmas</font></b></font> <font size="4">i</font><font
size="5">s</font> <font face="comic Sans MS"><font size="5">g</font><font size="4">o</font><font size="6">o<font size="8">o</font>o</font><font
size="4">o</font><font size="5">n</font><font size="5">n</font><font size="4">a</font></font><!--by doing this I make the word wabblelike-->
<i><font size="4">make <font face="Georgia">Clover</font></font></i> <b><font size="6"><font color="#ff0000">Bankcrupt!</font></font></b></h1>
<h3 align="center"><font size="5" face="comic Sans MS" color="#dd00dd">Am I Crazy to even think about going back to China for Christmas?? Wow,
even the plane ticket alone will cost me arms and legs! But, I do miss Xing very much, and miss my family!!</font></h3>
<h2 align="center"><font face="Georgia" color="#0000ee">Here goes my budget!</font></h2>
<h1 align="center"><font face="Times New Roman"
size="5">items                     &nb
sp;                      estimate
spend                       
                        
; purpose</font></h1>

<ul><!--this indicates I will make an unordered list-->
<center><li><font size="4" face="comic Sans MS">Plane ticket <!--this is a nonbreaking symbol--
>                       &nbs
p;           1,100
bucks                       
            I cannot walk back home! Can I??</font></center>
<center><li><font size="4" face="comic Sans
MS">Thinkpad~~~                     &n
bsp;          1,300
bucks                       
            For my dearest younger brother</font></center>
<center><li><font size="4" face="comic Sans
MS">Skincare~~~                     &n
bsp;            300
bucks                       
            For my mother and best friend</font></center>
<center><li><font size="4" face="comic Sans MS">NB
shoes~~~                      &nb
sp;           50 *5
bucks                       
            Mom, Dad, Grandpa, Xing, He</font></center>
<center><li><font size="4" face="comic Sans MS">UGA
mascots                      &nbs
p;           200
bucks                       
            For persons in my previous lab</font></center>
<center><li><font size="4" face="comic Sans
MS">foods&Snacks                     &
nbsp;            120
bucks                       
            For relatives and neighbours~</font></center>
</ul>
<br><!--this is a line break-->
<br>
<center><font size="4" face="Georgia" color="#0000ee">Is that All? Did I miss something?</font></center>
<center><font face="comic Sans MS" color="#ddoodd">Please, If you have any suggestions about my budget, sent me an <a
href="mailto:wanglilove2@gmail.com"><!--I add my email address link to my webpage--><font size="4">email!</font></font></a></center>

</body>
</html>
```

New Website, Comments, and Suggested Code:

Christmas is goOOoonna *make Clover* Bankcrupt!

Am I Crazy to even think about going back to China for Christmas?? Wow, even the plane ticket alone will cost me arms and legs! But, I do miss Xing very much, and miss my family!!

Here goes my budget!

Items	Estimated Cost	Purpose
Plane ticket	1,100 bucks	I cannot walk back home! Can I??
Thinkpad~~~	1,300 bucks	For my dearest, younger brother
Skincare~~~	300 bucks	For my mother and best friend
NB shoes~~~	50*5 bucks	Mom, Dad, Grandpa, Xing, He
UGA mascots	200 bucks	For people in my previous lab
Food & Snacks	120 bucks	For relatives and neighbors~

Is that All? Did I miss something?

Please, If you have any suggestions about my budget, sent me an email!

Comment: 2/2 on H3. Good work. Check out the following code. I used a table command instead of an unordered list (I think that it is easier than what you did with all the spaces). There might be an easier way to handle the fonts, but I am not that good at HTML.

```
<html><!--webpage begins with this tag-->
<head><!--head tag-->
<title>Clover's Christmas Budget</title><!--this is what will appear in the address bar-->
</head>
<body bgcolor="#ccffcc"><!--inside this tag you will write the contents of your webpage-->
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<i><font size="4">make <font face="Georgia">Clover</font></font></i> <b><font size="6"><font color="#ff0000">Bankcrupt!</font></font></b></h1>
<h3 align="center"><font size="5" face="comic Sans MS" color="#dd00dd">Am I Crazy to even think about going back to China for Christmas?? Wow,
even the plane ticket alone will cost me arms and legs! But, I do miss Xing very much, and miss my family!!</font></h3>
<h2 align="center"><font face="Georgia" color="#0000ee">Here goes my budget!</font></h2>
<table border="0" align="center" cellspacing="20" width="900">
<tr>
<th align="left"><font face="Times New Roman" size="5"><b>Items</th>
<th align="right"><font face="Times New Roman" size="5"><b>Estimated Cost</th>
<th align="right"><font face="Times New Roman" size="5"><b>Purpose</th>
</tr>
<tr>
<td align="left"><font size="4" face="comic Sans MS">Plane ticket</td>
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<td align="right"><font size="4" face="comic Sans MS">I cannot walk back home! Can I??</td>
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</tr>
<tr>
<td align="left"><font size="4" face="comic Sans MS">Skincare~~~</td>
<td align="right"><font size="4" face="comic Sans MS">300 bucks</td>
<td align="right"><font size="4" face="comic Sans MS">For my mother and best friend</td>
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<td align="right"><font size="4" face="comic Sans MS">Mom, Dad, Grandpa, Xing, He</td>
</tr>
<tr>
<td align="left"><font size="4" face="comic Sans MS">UGA mascots</td>
<td align="right"><font size="4" face="comic Sans MS">200 bucks</td>
<td align="right"><font size="4" face="comic Sans MS">For people in my previous lab</td>
</tr>
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<td align="left"><font size="4" face="comic Sans MS">Food & Snacks</td>
<td align="right"><font size="4" face="comic Sans MS">120 bucks</td>
<td align="right"><font size="4" face="comic Sans MS">For relatives and neighbors~</td>
</tr></font>
</table>
<br><!--this is a line break-->
<br>
<center><font size="4" face="Georgia" color="#0000ee">Is that All? Did I miss something?</font></center>
<center><font face="comic Sans MS" color="#ddoodd">Please, If you have any suggestions about my budget, sent me an <a
href="mailto:wanglilove2@gmail.com"><!--I add my email address link to my webpage--><font size="4">email!</font></font></a></center>
</body>
</html>
```

Innovative Teaching Activity

An increasingly important aspect of biology is the field of bioinformatics. Currently, many undergraduate biology programs do not have a bioinformatics component. I designed this activity to use web-based bioinformatics programs so students could solve an interesting, real-world problem that incorporates bioinformatics and evolutionary biology.

Phylogenetic Epidemiology

You are part of a team working for the Center for Disease Control in Atlanta, GA. There has been an outbreak of a disease in the Northeast. On June 12, 2010, 17 adolescent males at a boy scout camp in Milton, Massachusetts began suffering from headaches, fever, vomiting and drowsiness. Within days, 15 of the boys showed signs of confusion, respiratory distress and tremors. Encephalitis was found in the young men after a week. They began experiencing paralysis and five of the boys slipped into a coma. Two days after the onset of these symptoms, 13 of the boys died. The remaining four boys eventually recovered but still experience neurological damage.

An investigation into the region has revealed that this has happened before but never to the same severity. Cases dating back to May of 2009 show similar symptoms in individuals from Massachusetts, New York, Connecticut and New Hampshire.

The virus in question has had its genome sequenced from each of the victims from Milton, MA. You will find the complete sequence from one of the boys, identified as patient 0042, in the file marked "Unknown_42.fasta" on ELC.

You are tasked with the following:

1. Determine what the virus is or to what group of viruses it belongs.
2. Hypothesize how transmission of the virus occurs.
3. Postulate how to prevent infection and possible treatment of the virus.

Determining Taxonomic Identity of Virus

Using BLAST and Genbank

You will be using two tools that are vital to modern biology: BLAST and GenBank. BLAST is a program that takes your sequence of interest (in this case the viral genome) and uses it to search against a database of known sequences (GenBank). The results of the search are sequences that are very similar to the query sequence.

1. Go to http://blast.ncbi.nlm.nih.gov/Blast.cgi.
2. Click on "nucleotide blast". Either upload the virus genome file or copy and paste it into the box provided. Scroll down to "Database" and click "Others". The database "Nucleotide Collection" should be selected. Change from "megablast" to "blastn". Click "BLAST" to start the search.

3. Once the search is complete, answer the following questions:
   a. What are the top five hits for your sequence?
   b. What is the Max score, Query coverage and E-value for each of these hits?
   c. How would you use these to determine the identity of an unknown sequence?
4. Click on "Taxonomy reports".
   a. To what family of viruses does the unknown sample belong?
   b. What characteristics do members of this virus family share?
   c. For which well-known virus is the family named? What disease does it cause?

   d. What virus species is the best hit for the unknown sequence?

*******THE FOLLOWING WILL BE DONE FOR YOU BUT DISCUSSED IN CLASS*******

5. Go back to the BLAST results page. Scroll down and look at the query-subject alignments. Select all the alignments that have a Query coverage of more than 90% and click "Get selected sequences".
6. You will be directed to a Genbank page that has entry information for all of the selected sequences. Select them all again and click "Send to", then "File" and change format to "FASTA". Click "Create File".
7. Save the file as "Unknown_42_BLASThits.fasta".

****

8. Open the file and check to make sure it is in FASTA format:

>Sequence Name
AGATTTTCTTGCACGTGCGTGCGTTTGCTCCGGACAGCAACAGCAGCGACAGGTTTGAGAGAGGCGATCT
TTCGCTTGATCAGTCGTGAACGTGTTGAGAAAAAGACAGCTTAGGAGAACAAGAGCTGGGGATGGCCGGG
AAGGCCATTCTGAAAGGAAAGGGGGGCGGTCCTCCTAGACGAGTGTCGAAAGAGACCGCGAAGAAGACGC
GTCAATCTAGGGTCCAGATGCCAAATGGACTCGTGTTGATGCGCATGATGGGGATTTATGGCATGCCGT
AGCCGGCACTGCTAGAAGTCCCGTGTTGAAGTCTTTCTGGAATTCAGTTCCATTGAAACAGGCTACGGCA
GCACTCCGGAAGATCAAGAAGGCAGTGAGTACCCTGATGGTAGGTTTGCAAAGACGTGGTAAAAGGAGGT
>Sequence Name
GGAAAACAAATGTGCTCTGGTTCTTATGACGGCAACGCCACCAGGGAAGAGCGAACCCTTCCCAGAGTCC
AACGGAGCAATTACCAGTGAAGAGAAGCAGATCCCTGATGGGGAGTGGCGTGATGGGTTCGACTGGATCA
CCGAGTATGAGGGGCGCACCGCATGGTTCGTCCCCTCGATTGCAAAAGGTGGCATCATAGCCCGCACCCT
GAGACAAAAAGGAAAAAGTGTGATCTGTCTGAACAGCAAGACCTTTGAAAAGGACTACTCCAGAGTGAGA
GATGAGAAACCCGACTTCGTGGTCACAACCGACATATCTGAAATGGGGGCCAACCTCGATGTGAGCCGTG
TCATAGATGGGCGAACAAACATCAAACCGGAAGAGGTTGATGGGAGAGTTGAGCTCACAGGGACCAGAC

9. Copy and paste the unknown sequence to the BLAST hit file and save it.

Multiple Sequence Alignment: Using MUSCLE

You will now align the BLAST hits and unknown sequence using the program MUSCLE. There are a number of programs that can perform multiple sequence alignment. We are using MUSCLE because it is quick and fairly accurate.

10. Go to http://www.ebi.ac.uk/Tools/msa/muscle/.
11. Upload the file "Unknown_42_BLASThits.fasta". Click "Submit".
12. Click "View alignment". Copy and paste the alignment into a text document (use Notepad, Text Wrangler, etc.). Save the file as "Unknown_42_align.fasta".
13. Go to http://toolkit.tuebingen.mpg.de/alnviz and upload your alignment file. Make sure that FASTA format is selected before you click "Submit job".
14. Look over the alignment. Does it seem to make any major errors? If you are satisfied with the alignment, move on to the next step. If you are not satisfied, contact the instructor and explain why.
15. In order to do the phylogenetic analysis on the alignment, you will have to convert the FASTA alignment to a PHYLIP alignment. PHYLIP format has a limit of 10 characters to the name of each sequence. You will want to be able to identify your sequences after the conversion, so you will now shorten the names of your sequences so that the first 10 characters will allow them to be identified. Open your alignment file in Word (or some other document editor that has find/replace capability) and find/replace "gi |" with nothing. This should be enough so that the numerical identifier of the BLAST hits will be the names of the sequences when they are PHYLIP files. Save the file as plain text.
16. Go to http://www.ebi.ac.uk/cgi-bin/readseq.cgi. Upload the file you just saved and change the "Output sequence format" to Phylip 3.2. Submit your job.
17. When the job is finished, save the file as "Unknown_42_align.phy".
18. Open the PHYLIP alignment file in a text editor. You will notice that the format of this file (called Phylip format) is different from FASTA format.
    a. How do Phylip and FASTA formats differ (There are four ways.)?

Phylogenetic Reconstruction using Parsimony: dnapars from PHYLIP

You will be using a web-based version of the program dnapars from PHYLIP 3.67 to conduct a parsimony analysis of the unknown 42 sequence and your best BLAST hits.

19. Go to http://mobyle.pasteur.fr/cgi-bin/portal.py#forms::dnapars. Upload the PHYLIP alignment file you just created.

20. This first analysis is a search for the maximum parsimony tree. Change "Randomize input order" to "Yes". Select any odd number to seed the randomization process. Select any number of times to jumble to order of the taxa. Submit the job. You will be asked to enter an e-mail address with the submission. If you do not wish to use your own, you may use mrmckain.teaching@gmail.com.

21. The results page should come up quickly. Under "Outfile" click save. Name this file "Unknown_42_max_parsimonious". You can look at the output on the results page.

    a. How many most parsimonious trees are there?

    b. What is the total length of the maximum parsimony tree?

    c. Compare your maximum parsimony tree(s) length to those of your partners. Are they different? Why would they be different?

22. Look under the "Tree File" section. Save this as "Unknown_42_most_parsimonious_tree".

    a. Click on "view with archaeopteryx". Draw the tree. Do not wory about the branch lengths. Change the names from the GenBank IDs to the taxa names.

    b. What are branch lengths in a tree? What do they represent?

23. Exit out of the archaeopteryx viewer. Click "Back to form". Change randomize to "No". Change bootstrap to "Yes". Keep resampling methods on "Bootstrap" and number of replicates on "100". Select an odd number to seed the process. Submit the job.

24. When the results page comes up, scroll down to "Consense tree file". Save the consense.outtree to a file called "Unknown_42_parsimony_bootstrap_tree".

    a. What type of consensus is this? Look at the consensus outfile to find out.

    b. What does this mean?

25. View the consensus tree using archaeopteryx. Draw the tree including bootstrap values. Change the names from the GenBank IDs to the taxa names.

    a. Branch lengths have no meaning in consensus trees. Why do you think that is?

    b. Do the consensus and maximum parsimony trees have the same root? If not, click on "Click on Node to" and change it to "Root/Reroot". Click on the node that will give the consensus tree the same root at the maximum parsimony tree. Redraw the here.

26. Compare and contrast the consensus and maximum parsimony trees.

    a. How many differences do you see between the two trees?

    b. What are they?

    c. Does the placement of the Unknown_42 virus change between the two trees? If yes, how so?

    d. To what is the Unknown_42 virus most closely related?

    e. How confident are you in that conclusion?

    f. How did you measure your confidence in the above answer?

    g. Was the most closely related GenBank sequence (based on phylogeny) also the best hit from BLAST? If it was not, why do you think this is so?

27. Use the Internet to answer the following questions about the closest relative to the unknown virus.

    h. To what family does the virus belong?

    i. Where does the virus originate?

    j. How is the virus transmitted to humans?

    k. What are the symptoms of infection?

    l. What is the virulence of the virus measured in mortality?

Professional Activities Related to Teaching

UGA Outstanding TA Award, Spring 2011

UGA Future Faculty Program, 2011-2012

Course Design—Graduate Student Seminar in Teaching, Fall 2011
I was a co-instructor for a course designed to prepare new graduate students to be teachers at UGA. As the student co-instructor, I was tasked with designing the entire course based on a set of criteria from the Graduate School. Students were introduced to various teaching techniques, provided information on services available at UGA and given the opportunity to practice making assessments/rubrics and giving lectures. Based on an evaluation I gave the class the previous year, I introduced active learning strategy techniques to the class and gave the students the opportunity to create their own and implement them.

Peer Teaching Evaluator—2011-2012
As an elected position of the Plant Biology Graduate Student Association, I am responsible for providing assistance, advice, information and evaluation of teaching methods and opportunities for the graduate students in the Department of Plant Biology. I also provide students with help in creating their Teaching Portfolios for submission to the Graduate School.

Class Module Development—BIOL 2108H: Principles of Biology II, Spring 2011
In collaboration with Dr. Paula Lemons, I created a two class period module that taught underclassmen how to use bioinformatics tools available on the Internet. Bioinformatics is increasingly important in modern biology research but it is not currently part of most biology curricula. This module allowed students to answer a real-world question focused on epidemiology and to explore techniques that are used by researchers. Students were very interested in the application of bioinformatics to issues concerning human health.

The module's success interested Prof. Mark Farmer who had me modify the module to a single class period for his HONS 2080H: Honors Science non-majors class. The module proved successful in this course as well.

Teaching Outreach—Hilsman Middle School, Spring 2011-2012
I have developed working with approximately 4-5 other students from Plant Biology an outreach course that teaches 7th grade students at Hilsman Middle School various aspects of plant biology. This includes going into the two agriscience classes of Dr. Pam Stratton once a week to teach the students about plant genetics, taxonomy, domestication and ecology. We also provide the opportunity for the students to do genetic cross experiments using Wisconsin Fast Plants. Students present their work in poster presentations at the end of the semester. In addition to teaching, we are developing teaching, native and community gardens on the Hilsman Middle School property to aid in teaching the students about domestication, native plants and proper nutrition.

Teaching, Mentoring and Training Experiences

Courses taken at University of Georgia designed for future college teachers.

Fall 2010	GRSC 7900: Designing Courses for Significant Learning Purpose of course is to give graduate students a strong foundation in course design and pedagogical theory. Students design an entire course over the semester. This was the first time I designed a course and it was very helpful when I designed and taught my first class as a co-instructor.
Spring 2010	GRSC 7800: College Teaching and Student Learning Purpose of course is to explore how undergraduate learn. Focus is on how to be an effective college teacher through exploring what factors influence teaching and learning. This course served as an advanced pedagogy course that introduced me to active learning strategies.
Fall 2007	GRSC 7770: Graduate Seminar Purpose of course is to provide new teaching assistants with pedagogical approaches to teaching and support systems provided by the University. This was my first introduction to teaching.

MENTORING EXPERIENCE

2010-2011	Student: Julianah Ayeni Project Title: Plastid Genome Variation in the Monocots I taught Julianah bioinformatics techniques used to assemble and analyze data. We also discussed trends in the evolution of monocot plastid genomes and used some of her data in published research.
2009-2010	Student: Nick Dallas Project Title: Genetic Diversity of *Yucca filamentosa* and *Y. aloifolia* in Athens-Clarke County, Georgia Nick's project was one that I designed. I gave him options for possible projects and he chose this particular one. In it, I taught him how to conduct fieldwork, DNA isolation, PCR amplification, sequencing and phylogenetic analyses. Nick ultimately presented his work at the CURO symposium in Spring 2010.

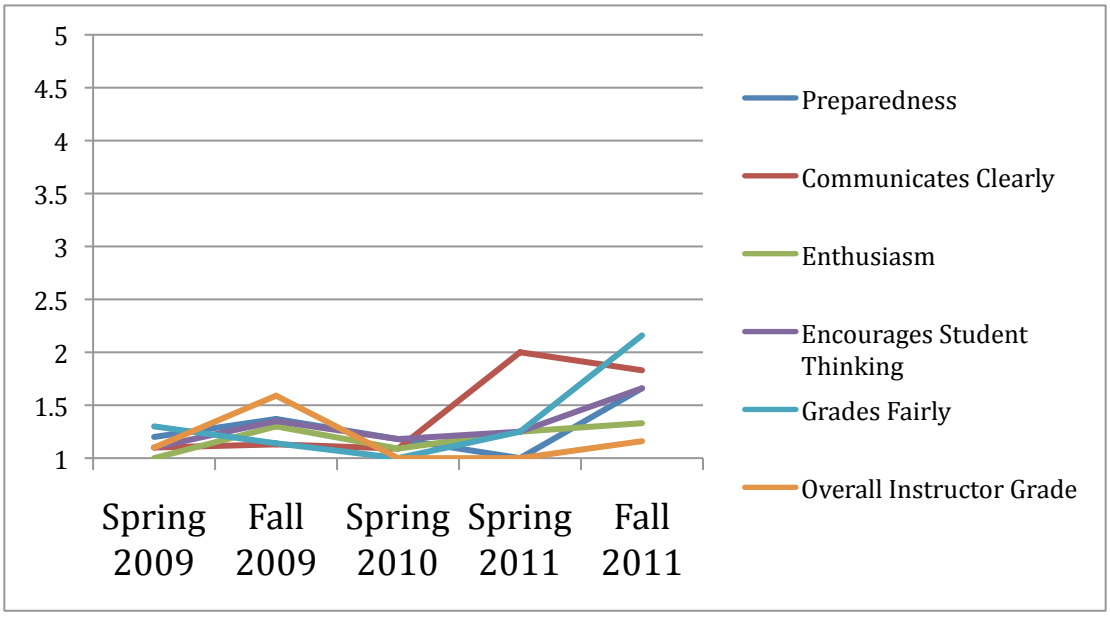
Summary of Teaching Evaluations

During my time as a graduate student, the evaluations for courses changed. Evaluations for Spring 2011 and Fall 2011 are based on a different questionnaire and different scoring system that I have adjusted to fit the old evaluation style. All original evaluations are available upon request.

Courses Taught:
Spring 2009, Spring 2011: PBIO 4650L/6650L—Plant Taxonomy
Fall 2009: PBIO-BIOL-BINF 4550/6550—Bioinformatics Applications
Spring 2010: PBIO 6350L—Molecular Systematics
Fall 2011: GRSC 7770—Graduate Student Teaching Seminar

Quantitative Student Evaluation Summary

Scores are based on a 1-5 system, where 1 is the best and 5 the worst.



Quantitative Student Evaluation Summary

Michael is very good at explaining clearly how to perform certain tasks and is always incredibly helpful. He goes out of his way to be helpful and has a very solid foundation with respect to knowledge about the material/class. He is a great instructor.

He is very understandable. I frequently got lost in lecture and Michael was always able to straighten things out.

He explains very well. Easily approachable. Knows content well. Excellent TA had so far in my coursework.

Encourage thought among students. Enthusiastic. Fair grades.

Michael has patience . . . I would not have had the patience with some students that he had. Keep up your laid-back attitude – it is helpful when learning hundreds of names and terms!

Patiently works with students who are having a difficult time with the course material. He is always willing to help, and if he is unsure about any of the information being taught, he admits it and informs the class of the corrections promptly.

ALL of the TAs (Michael, Pat, and Ling) deserve recognition for the time and effort they put in to this course. Their dedication to teaching was evident, and they often went above and beyond what was required of them to ensure their students were learning.

Michael really wants to help us learn and understand, and is very willing to answer any questions.

Help students with individual problems and being available for questions inside and outside of class.

Michael makes class fun and interesting. He makes sure to keep us aware of WHY we are learning/doing certain things, even though much of the subject material isn't yet immediately relevant to many of us. The loose, discussion-based format works well, as we feel comfortable trying out different teaching strategies in a safe space.

I was co-instructor with Michael for a semester in a course designed to prepare life science graduate students to serve as teaching assistants. Michael developed the course and ran it, my role was really more that of a consultant. Michael's enthusiasm for teaching and for student involvement really came through in the course. His greatest strength was actively engaging the students--he made them feel comfortable and valued their ideas, which in turn encouraged their participation. –Prof. Michelle Momany

When my department head suggested that I co-teach a course on teaching methods and pedagogy theory to incoming grad students, I was a little trepidatious since I didn't have very much teaching experience myself. Fortunately for me, my co-instructor was Michael, who handled all aspects of designing the course, leading the class discussions, and assessing the students - in other words, although we are both listed as co-instructors on the books, Michael did 99.9% of the effort in teaching this course, while I threw out occasional comments from the peanut gallery. Having observed Michael in the classroom for a whole semester, I found him to be unusually effective in drawing out the participation of the students and fostering sophisticated discussions. Michael has a particular passion for active learning strategies, and he passed this on to the students both by modeling how to use them effectively throughout the semester as well as encouraging the students to develop their own activities. Michael set a comfortable, collaborative tone to the course from the first day, and maintained a non-judgmental atmosphere throughout the semester that allowed for the particularly engaged student dynamic. In short, I found Michael to be both dedicated to job of teaching and talented in the art of teaching, skillfully combing the current theories on how students learn, practical approaches to applying those theories to the classroom, and a sympatico with the students that allowed those practices to be successful. –Assist. Prof. Rick Lankau

I had my GRSC 7770 students do a second course evaluation using questions I wrote. They completed this while I was out of the room and we came together to talk about it. This is the concept map they created describing the course: